SEQUENCE LISTING

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<120>   Vectors for Gene Mutagenesis and Gene Discovery

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<140>   US 09/443,282
<141>   1999-11-19

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<151>   1999-03-25

<150>   US 60/109,302
<151>   1998-11-20

<150>   US 60/081,727
<151>   1998-04-14

<150>   US 60/079,729
<151>   1998-03-27

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<170>   PatentIn version 3.2

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tactaacatt gccttttcct ccttccctcc cacaggt                       37


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ctctctgcct attggtctat tttcccaccc ttaggc                        36


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aagcccggtg cctgactagc tag                                          23


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gaatatgtct ccaggtccag ag                                           22


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ccagtgagca gagtgacgag gac                                          23


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<400>  16
ctagctaggg agctcgtc                                                18


<210>  17
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<400>  17
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ccagagtctt cagagatcaa gtc                                              23


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<400>   18
gaggactcga gctcaagc                                                    18


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<400>   19
ctgtaaaacg acggccagtc                                                  20


<210>   20
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cagacgtg                                                               68


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<400>   21
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cagacgug                                                               68


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ugcagacgug                                                                 70


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aggagaggag aggagaggag aggagaggag aggagaggag aggagaggag aggagatctc       180

aggtgagttc gcatgtgctt cgaacttgtg tgcatgcgtt ctaaaagggc ttctcttggt       240

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<213>  Artificial Sequence

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<400>  25
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ggagaggaga ggagaggaga tctcaggtga gttcgcatgt gctt                        104


<210>  26
<211>  96
<212>  DNA
<213>  Artificial Sequence

<220>
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<400>  26
atgtggaaga gctcgggtac caggagagga gaggagagga gaggagagga gaggagagga        60
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gaggagagga gatctcaggt gagttcgcat gtgctt   96

<210> 27
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<213> Artificial Sequence

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<220>
<221> misc_feature
<222> (20)..(518)
<223> n = a, t, c, or g

<220>
<221> misc_feature
<222> (20)..(518)
<223> each of these residues may be absent or present

<400> 27
gtggaagagc tcgggtaccn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   120

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   180

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   420

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   480

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnntc tcaggt   526

<210> 28
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<220>
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<222> (22)..(520)
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<220>
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<223> each of these residues may be absent or present

<400> 28
atgtggaaga gctcgggtac cnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   120

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   180

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   420

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   480

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn tctcaggt   528

<210>   29
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<220>
<221>   misc_feature
<222>   (22)..(520)
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<223>   n = a, t, c, or g

<220>
<221>   misc_feature
<222>   (22)..(520)
<223>   each of these residues may be absent or present

<400>   29
atgtggaaga gctcgggtac cnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   120

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   180

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   420

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   480

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn tctcaggt   528

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atctcaggt                                                                69


<210>   31
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tgagttcgca tgtgctt                                                       77


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<220>
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<223>   Sequence "agagg" repeats 1-50 times, maximum number of repeats
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gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga       120

gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga       180

gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga       240

gaggagagga gagggagttc gcatgtgctt                                        270


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gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga      120

gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga      180

gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga gaggagagga      240

gaggagagga gagg                                                        254
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